



MET SER LEU LEU THR GLU VAL GLU THR PRO ILE  
A T G A G C C T T C T A A C C G A G G T C G A A A C . . . A C C T A T  
T A C T C G G A A G A T T G G C T C C A G C T T T G . . . T G G A T A  
10 20 720

ARG ASN GLU TRP GLU CYS ARG CYS ASN GLY  
C A G A A A C G A A T G G G A G T G C A G A T G C A A C G G  
G T C T T T G C T T A C C C T C A C G T C T A C G T T G C C  
730 740 750

SER SER ASP PRO LEU VAL VAL ALA ALA SER  
T T C A A G T G A C C C G C T T G T T G T T G C T G C G A G  
A A G T T C A C T G G G C G A A C A A C A A C G A C G C T C  
760 770 780

ILE ILE GLY ILE LEU HIS LEU ILE LEU TRP  
T A T C A T T G G G A T C T T G C A C T T G A T A T T G T G  
A T A G T A A C C C T A G A A C G T G A A C T A T A A C A C  
790 800 810

ILE PHE ASP ARG LEU PHE PHE LYS CYS ILE  
G A T T T T T G A T C G T C T T T T T T T C A A A T G C A T  
C T A A A A A C T A G C A G A A A A A A A G T T T A C G T A  
820 830 840

TYR ARG LEU PHE LYS TYR GLY LEU LYS ARG  
C T A T C G A C T C T T C A A A T A C G G T C T G A A A A G  
G A T A G C T G A G A A G T T T A T G C C A G A C T T T T C  
850 860 870

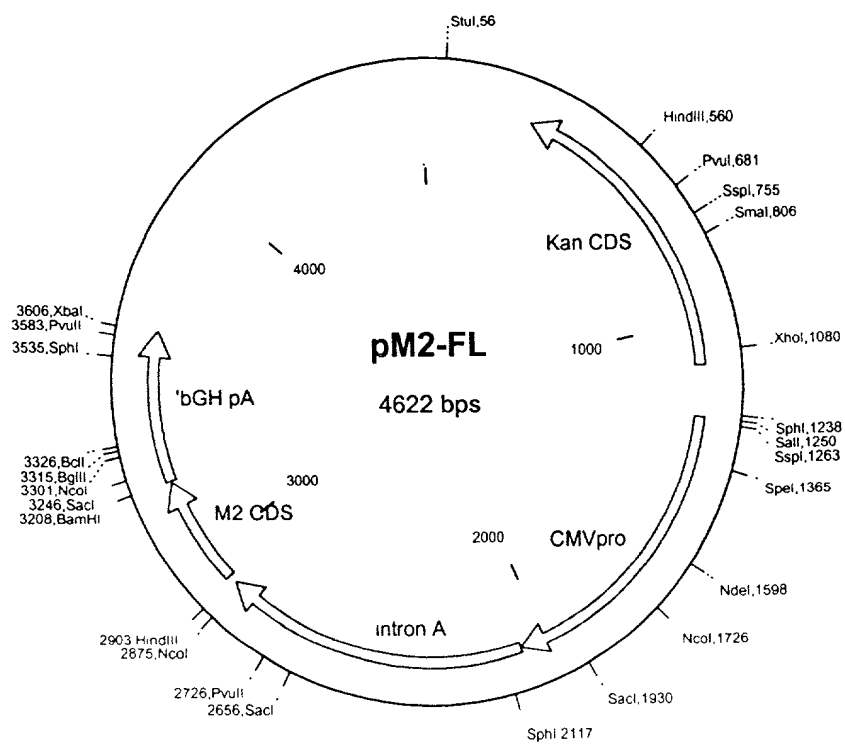
GLY PRO SER THR GLU GLY VAL PRO GLU SER  
A G G G C C T T C T A C G G A A G G A G T A C C T G A G T C  
T C C C G G A A G A T G C C T T C C T C A T G G A C T C A G  
880 890 900

MET ARG GLU GLU TYR ARG LYS GLU GLN GLN  
T A T G A G G G A A G A A T A T C G A A A G G A A C A G C A  
A T A C T C C C T T C T T A T A G C T T T C C T T G T C G T  
910 920 930

ASN ALA VAL ASP ALA ASP ASP SER HIS PHE  
G A A T G C T G T G G A T G C T G A C G A C A G T C A T T T  
C T T A C G A C A C C T A C G A C T G C T G T C A G T A A A  
940 950 960

VAL SER ILE GLU LEU GLU \*\*\*  
T G T C A G C A T A G A G C T G G A G T A A  
A C A G T C G T A T C T C G A C C T C A T T  
970 980

Figure 2



**Figure 3**

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1 GGGGCGGGG GGCGCTGAG TGTGCCTCGT GAAGAAGGTG TTGCTGACTC ATACCAGGCC TGAATCGCCC CATCATCCAG CCAGAAAGTG
      |
91 AGGGAGCCAC GTTGATGAG AGCTTTGTTG TAGTGGGACC AGTTGGTGAT TTTGAACITT TGCTTTGCCA CGGAACGGTC TCGTGTGTCG

181 GGAAGATGCG TGATCTGATC CTTCAACTCA GCAAAGATTG GATTATTCCA ACAAAGCCGC CGTCCCGTCA AGTCAGCGTA ATGCTCTGCC

271 AGTGTACAAA CCAATAACC AATTCTGATT AGAAAAACTC ATCGAGCATC AAATGAACT GCAATTATT CATATCAGGA TTATCAATAC
      <<.....Kan CDS.....>>

361 CATATTTTTG AAAAAGCCGT TTCTGTAATG AAGGAGAAAA CTCACCGAGG CAGTTCCATA GGATGGCAAG ATCTCGGTAT CGGTCTGCGA
< .....Kan CDS.....>

451 TTCGACTCG TCACAACATCA ATACAACCTA TTAATTTCCC CTGTCACAAA ATAAGTTTAT CAAGTGAGAA ATCACCATGA GTGAGGACTG
< .....Kan CDS.....>

541 AATCCGGTGA GAATGGCAAA AGCTTATGCA TTTCTTTCCA GACTTGTICA ACAGGCCAGC CATTACGCTC GTCATCAAAA TCACTCGCAT
< .....Kan CDS.....>

631 CAACCAAACG GTTATTCATT CGTGATTGCG CCTGAGCGAG ACGAAATACG CGATCGCTGT TAAAAGGACA ATTACAACA GGAATCGAAT
< .....Kan CDS.....>

721 GCAACCGGCG CAGGAACACT GCCAGCGCAT CAACAATATT TTCACCTGAA TCAGGATATT CTTCTAATAC CTGGAATGCT GTTTCCCGG
< .....Kan CDS.....>

811 GGATCGCAGT GGTGAGTAAC CATGCATCAT CAGGAGTAGC GATAAAATGC TTGATGGTCG GAAGAGGCAT AAATCCGTC AGCCAGTTTA
< .....Kan CDS.....>

901 GTCTGACCAT CTCATCTGTA ACATCATTGG CAACGCTACC TTTGCCATGT TTCAGAAACA ACTCTGGCGC ATGGGGCTTC CCATACAATC
< .....Kan CDS.....>

991 GATAGATTGT CGCACTGAT TGCCCGACAT TATCGCGAGC CCATTTATAC CCATATAAAT CAGCATCCAT GTTGGAATTT AATCGCGGCC
< ..... Kan CDS .. ...>

1081 TCGAGCAAGA CGTTTCCCGT TGAATATGCG TCATAACACC CTTTGTATTA CTGTTTATGT AAGCAGACAG TTTTATTGTT CATGATGATA
< Kan CDS .. <<

1171 TATTTTATC TTGTGCAATG TAACATCAGA GATTTGAGA CACAACGTGG CTTCCCCCCC CCCCCGGGCA TGCCTGCAGS TCGACATAAA
>>CMVpro >

1261 TCAATATTGG CTATTGGCCA TTGCATACGT TGTATCTATA TCATAATATG TACATTTATA TTGGCTCATG TCCAATATGA CCGCATGTT
> CMVpro >

1351 GACATTGATT ATTGACTAGT TATTAATAGT AATCAATTAC GGGGTCTTAA GTTCATAGCC CATATATGGA GTTCCGCGTT ACATAACTTA
> CMVpro ....>

1441 CGGTAAATGG CCCGCCTCGT GACCGCCCAA CGACCCCGCG CCATTGACGT CAATAATGAC GTATGTTCCC ATAGTAACGC CAATAGGGAC
> CMVpro....>

1531 TTTCCATTGA CGTCAATGGG TGGAGTATTT ACGGTAAACT GCCCACTTGG CAGTACATCA AGTGTATCAT ATGCCAAGTC CGGCCCCCTA
> CMVpro . . .>

1621 TTGACGTCAA TGACGGTAAA TGGCCCGCCT GGCATTATGC CCAGTACATG ACCTIACGGG ACTITCTTAC TTGGCAGTAC ATCTACGTAT
> CMVpro >

1711 TAGTCAICGC TATTACCATG GTGATGCGGT TTTGGCAGTA CACCAATGGG CGTGGATAGC GGTITGACTC ACGGGGATTT CCAAGICTCC
> CMVpro >

1801 ACCCCATTGA CGTCAATGGG AGTTTGTITT GGCACCAAAA TCAACGGGAC TTTCACAAAT GTCGTAATAA CCCCCCCCCG TTGACGCAAA
> CMVpro
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1891 TGGGCGGTAG GCGGTACGG TGGGAGGTCT ATATAAGCAG AGCTCGTTTA GTGAACCGTC AGATCGCCTG GAGACGCCAT CCACGCTGTT  
> .....CMVpro. ....>

1981 TTGACCTCCA TAGAAGACAC CGGGACCGAT CCAGCCTCG CGGCCGGAA CGGTGCATTG GAACGCGGAT TCCCCGTGCC AAGAGTGAAG  
> .....CMVpro.....>>

2071 TAAGTACCGC CTATAGACTC TATAGGCACA CCCCTTTGGC TCTTATGCAT GCTATACTGT TTTTGGCTTG GGGCCTATAC ACCCCGCTC  
> .....intron A.....>

2161 CTTATGCTAT AGGTGATGGT ATAGCTTAGC CTATAGGTGT GGGTATTGA CCATTATTGA CCACTCCCCT ATTGGTGAGC ATACTTTCCA  
> .....intron A.....>

2251 TTACTAATCC ATAACATGGC TCTTTGCCAC AACTATCTCT ATTGGCTATA TGCCAATACT CTGTCCTTCA GAGACTGACA CGGACTCTGT  
> .....intron A.....>

2341 ATTTTACAG GATGGGGTCC CATTATTAT TTACAAATC ACATATACAA CAACGCCGTC CCCCGTGCCC GCAGTTTTTA TTAACATAG  
> .....intron A.....>

2431 CGTGGGATCT CCACGCGAAT CTCGGGTACG TGTCCGGAC ATGGGCTCTT CTCCGTAGC GCGGAGCTT CCACATCGA GCCCTGGTC  
> .....intron A.....>

2521 CATGCCTCCA GCGGCTCATG GTCGCTCGC AGTCCTTGC TCCTAACAGT GGAGGCCAGA CTTAGGCACA GCACAATGCC CACCACCACC  
> .....intron A.....>

2611 AGTGTGCCG ACAAGGCCGT GCGGGTAGGG TATGTGTCTG AAAATGAGCT CGGAGATTGG GCTCGCACC TGACGCAGAT GGAAGACTTA  
> .....intron A.....>

2701 AGGCAGCGC AGAAGAAGAT GCAGGCAGCT GAGTTGTGT ATTCTGATAA GAGTCAGAG TAACCTCCGT TCGGTGCTG TTAACGGTG  
> .....intron A.....>

2791 AGGGCAGTGT AGTCTGAGCA GTACTCGTTG CTGCCGCGC CGCCACCAGA CATAATAGCT GACAGACTAA CAGACTGTTC CTTTCCATG  
> .....intron A.....>

2881 GTCTTTTCTG CAGTCACCGT CCAAGCTTCC ACCATGAGCC TTCTAACCGA GTCGAAACA CCTATCAGAA ACGAATGGGA GTGCAGATG  
> .....intron A >> .....M2 CDS.....>

2971 AACGGTTCAA GTGACCCGCT TGTGTGTCT GCGAGTATCA TTGGGATCTT GCACTTGATA TTGTGGATT TTGATCGTCT TTTTTCAAA  
> .....M2 CDS.....>

3061 TGCATCTATC GACTCTTCAA ATACGGTCTG AAAAGAGGGC CTCTACGGA AGGAGTACCT GAGTCTATGA GGAAGAATA TCGAAAGGAA  
> .....M2 CDS.....>

3151 CAGCAGAATG CTGTGGATGC TGACGACAGT CATTTTGTCA GCATAGAGCT GGAGTAAGGA TCCTCGCAAT CCTAGGAGG ATTAGGCAAG  
> .....M2 CDS.....>> .....bGH pA.....>

3241 GGCTTGAGCT CACGCTCTTG TGAGGGACAG AAATACAATC AGGGGCAGTA TATGAATACT CCATGGAGAA ACCCAGATCT ACGTATGATC  
> .....bGH pA.....>

3331 AGCCTCGACT GTGCCTTCTA GTTGCCAGCC ATCTGTTGTT TGCCCTTCCC CCGTGCCTTC CTTGACCCTG GAAGGTGCCA CTCCTACTGT  
> .....bGH pA.....>

3421 CTTTCTTAA TAAATGAGG AAATTGCATC GCATTGTCTG AGTAGGTGTC ATTCTATTCT GGGGGTGGG GTGGGGCAGG ACAGCAAGGG  
> .....bGH pA.....>

3511 GGAGGATTGG GAAGACAATA GCAGGCATGC TGGGGATGCG GTGGGCTCTA TGCTTCTGA GCGGAAAGA ACCAGCTGG GCTCGACAGC  
> .....bGH pA.....>

3601 TGGACTCTAG AATTGCTTCC TCGCTCACTG ACTCGCTGCG CTCGTCGTT CGGCTGCGC GAGCGGTATC AGCTCACTCA AAGGCGGTAA  
> .....bGH pA >>.....>

3691 TACGGTTATC CACAGAATCA GGGGATAACG CAGGAAAGAA CATGTGAGCA AAAGGCCAGC AAAAGGCCAG GAACCGTAAA AAGGCCGCGT  
3781 TGCTGGCGTT TTTCCATAGG CTCCGCCCCC CTGACGAGCA TCACAAAAT CGACGCTCAA GTCAGAGGTG GCGAAACCG ACAGGACTAT  
3871 AAAGATACCA GCGTTTTCCC CCTGGAAGCT CCCTCGTGCG CTCTCTGTT CCGACCCCTGC CGCTTACCGG ATACCTGTCC GCCTTTCTCC  
1961 CTTGGGAAG CGTGGCGCTT TCTCAATGCT CACGCTGTAG GTATCTCAGT TCGGTGTAGG TCGTTCGCTC CAAGCTGGGC TGTGTGCACG  
4051 AACCCCCCGT TCAGCCCGAC CGCTGCGCTT TATCCGATA CTATCGTCTT GAGTCCAACC CGGTAAGACA CGACTTATCG CCACTGGCAG  
4141 CAGCCACTGG TAACAGGATT AGCAGAGCGA GGTATGTAGG CGGTGCTACA GAGTTCTTGA AGTGGTGGCC TAACTACGGC TAACTAGAA  
4231 GGACAGTATT TGGTATCTGC GCTCTGCTGA AGCCAGTTAC CTTGGAAAA AGAGTTGGTA GCTCTTGATC CGGCAAAACA ACCACCGCTG  
4321 GTAGCGGTGG TTTTTTGTG TGCAAGCAGC AGATTACGCG CAGAAAAAAA GGATCTCAAG AAGATCCTTT GATCTTTTCT ACGGGGTCTG  
4411 ACGCTCAGTG GAACGAAAAC TCACGTTAAG GGATTTTGGT CATGAGATTA TCAAAAAGGA TCTTCACCTA GATCCTTTTA AATTAAAAAT  
4501 GAAGTTTAA ATCAATCTAA AGTATATATG AGTAAACTTG GTCTGACAGT TACCAATGCT TAATCAGTGA GGCACCTATC TCAGCGATCT  
4591 GTCTATTTTC TTCATCCATA GTTGCCTGAC TC

**Figure 4**

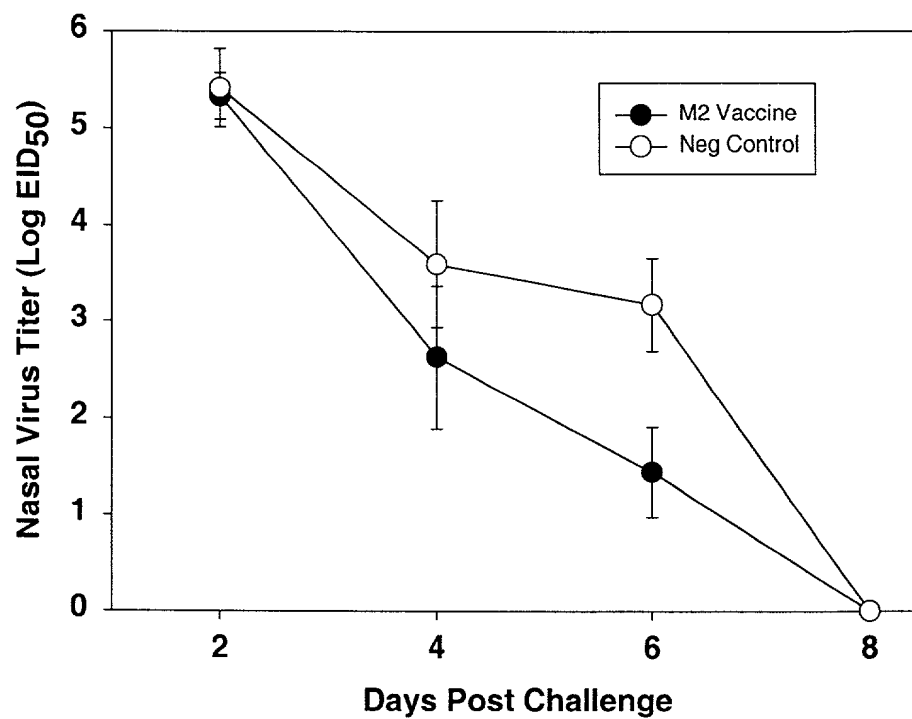


Figure 5